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Db 1245 -----TCACTCAAGAGGGCTTCAAGCCGTG 1271
Qy 284 SerGuseRAlaAlaLeuArgGlnArg-----GluYr 294
Db 1272 GCGTCTCGGCTCACTGAGAGAGGCAATGCTGTCCAGAGCTTCAAGCCAGCC 1331
Qy 295 AlaGluLeuLeuArgGlyArgGlyLeuAlaArgSerLeuAlaIleLeuSerAlaPhe 314
Db 1332 TTTCGGCTGTCTCGGAGACAGGAAAGTGGCAAGTCCGCGCCCTCACTCGAGCATCTTT 1391
Qy 315 AlaIleCysTrpAlaProGlyCysLeuPheThrIleValLeuSerThrYrProArgThr 334
Db 1392 GCGCTCTCGGCTCGGCTCAAGCTCTGATATATATATCCGAGCCGCTGCAAGCCAC 1451
Qy 335 GluArgProLySerValTrpYrSerIleAlaPheTrpLeuGlnTrpPheAlaSerPhe 354
Db 1452 TGCCTCTCT---GACTACTGATACGAAACCTCTCTGCTCTGCTGCGCCAACTCGGCT 1508
Qy 355 ValAlaProPheLeuTrpProLeuCysHisArgArgPheGlnIleValAlaPheTrpYrIle 374
Db 1509 GTCAACCTGTCTCTACCTCTGTGTCACACAGCTTCCGCGGCTTCAAGCAAGCTG 1568
Qy 375 LeuCysValThrYr-----Trp-----380
Db 1569 CTGCGCCCAAGAGCTCAAAATTCAGCCCAAGCTCTCGAGCATCTCGAAGTGA 1628
Qy 381 -----ProAlaLeuSerGlnAlaGlnSer 388
Db 1629 GTGCGCCCAAGAGCTCTCTCAAGCCAGCTCTCTCAAGCCAGCTG 1676

RESULT 5
US-09-165-543-1
Sequence 1, Application US/09165543
GENERAL INFORMATION:
PATENT NO. 6083545
APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESS: LAMIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: NNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)237-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS

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! LOCATION: 291..1625
US-09-165-543-1
Alignment Scores:
Pred. No.: 4,87e-65
Score: 724.50
Percent Similarity: 48.90%
Best Local Similarity: 37.50%
Query Match: 35.38%
DB: 3
Gaps: 12

US-10-626-445-8 (1-391) x US-09-165-543-1 (1-2689)
Qy 18 LeuAlaPheLeuMetSerSerPheAlaIleMetValGlyValAlaValIle 37
Db 399 CTGGCCGCGCTCATGGCGCTGCTCATCTGCGCCAGCTGCGCAAGCTGCTGATG 458
Qy 38 LeuAlaPheValAlaPArgAlaMetLeuArgHisArgSerAlaTrpPhePheLeuAlaLeu 57
Db 459 CTGCGCTTGTGGCGGACGACGAGCTCGGACCCAGAAACATCTTCTCTCAAGCTC 518
Qy 58 AlaIleSerAlaPheLeuValGlyLeuIleSerIleProLeuTrpIleProHisValLeu 77
Db 519 GGCATCTCGACCTCTCTGCTGCTGCGCTTGCATCTCACTGATGATACCTTACCTG 578
Qy 78 Phe---AenTrpAlaPheGlySerGlyIleCysMetPheTrpLeuIleThrAepTrpLeu 96
Db 579 ACAAGCCGCTGACCTTCCGCGCGGCTCTGCAAGCTGCTGCTGATGATGATACCTG 638
Qy 97 LeuCyethAlaSerValTrpAlaIleValIleLeuIleSerTrpAlaPArgTrpAlaSerVal 116
Db 639 CTGTGCACTCTCTCTGCTCAATGCTGCTATGCTATGATGATGATGATGATGATG 698
Qy 117 SerAlaValAlaSerTrpAlaGlnIleThrGlyIleMetLeuIleValAlaGlnMet 136
Db 639 ACCGAGCGGTCTATACCGGCGGCGGAGGTGACCGCGGCGGAGTGGAGAAAGTG 758
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAlaGlnIlePrometIleAlaIleSerAepSer 156
Db 759 CTGCTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 809
Qy 157 TrpYr-----AenSerThrAenThrIleAepCysGluProGlyPheVal 171
Db 810 TGGGATGACTGCTCGGCGGCGGCTCATCCGAGGCGGCACTGCTGATGCGAGTCTTC 869
Qy 172 ThrGluTrpYrIleLeuThrIleThrMetLeuGluPheLeuLeuProValIleSer 191
Db 870 TACAACCTGTACTTCTCATACGCGCTTCCACCTGAGATCTTACCCCTTCTCAGC 929
Qy 192 ValAlaTrpPheAlaValGlnIleTrp-----200
Db 930 GTCACTTCTTAACTACACATCTACGAAATTCAGAGCGGACCCGCTCGGCTG 989
Qy 200 -----200
Db 990 GATGGGCTCGAGAGGAGCGGCGGCGGCGGCTTCCGAGGCGGACCTTCAAGCC 1049
Qy 201 -----TrpSerLeuTrpYrArgArgAlaLeuSerArgCysProSerHis 215
Db 1050 CCACGCGCTGCTCTGCGGCTGCTGCGAGAGGCGGAGGAGGAGGAGGAGGAGGAGG 1109
Qy 216 -----AlaGlyPheSerThrHisSerSer 223
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Qy 224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgTrpSerAlaProGlyLeu 243
Db 1170 GCGGATGGAGGCT-----GGCTCGTGGCTTCAAGCCACCTTCCAGCTCGGCTG 1214
Qy 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgIleSerSerIleLeuVal 263
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